

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: BAICHWAL, VIJAY R
HUANG, JIANING
5 HSU, HAILING
GOEDDEL, DAVID V

(ii) TITLE OF INVENTION: RIP: NOVEL HUMAN PROTEIN INVOLVED IN
TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING
ASSAYS

10 (iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
(B) STREET: 75 DENISE DRIVE
(C) CITY: HILLSBOROUGH
15 (D) STATE: CALIFORNIA
(E) COUNTRY: USA
(F) ZIP: 94010

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
20 (B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
25 (B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: OSMAN, RICHARD A.
(B) REGISTRATION NUMBER: 36,627
30 (C) REFERENCE/DOCKET NUMBER: T95-006-1

(ix) TELECOMMUNICATION INFORMATION:

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35 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2016 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 1..2013

(x1) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	ATG CAA CCA GAC ATG TCC TTG AAT GTC ATT AAG ATG AAA TCC AGT GAC	48
	Met Gln Pro Asp Met Ser Leu Asn Val Ile Lys Met Lys Ser Ser Asp	
	1 5 10 15	
5	TTG CTG GAG AGT GCA GAA CTG GAC AGC GGA GGC TTT GGG AAG GTG TCT	96
	Phe Leu Glu Ser Ala Glu Leu Asp Ser Gly Gly Phe Gly Lys Val Ser	
	20 25 30	
	CTG TGT TTC CAC AGA ACC CAG GGA CTC ATG ATC ATG AAA ACA GTG TAC	144
	Leu Cys Phe His Arg Thr Gln Gly Leu Met Ile Met Lys Thr Val Tyr	
10	35 40 45	
	AAG GGG CCC AAC TGC ATT GAG CAC AAC GAG GCC CTC TTG GAG GAG GCG	192
	Lys Gly Pro Asn Cys Ile Glu His Asn Glu Ala Leu Leu Glu Glu Ala	
	50 55 60	
15	AAG ATG ATG AAC AGA CTG AGA CAC AGC CGG GTG GTG AAG CTC CTG GGC	240
	Lys Met Met Asn Arg Leu Arg His Ser Arg Val Val Lys Leu Leu Gly	
	65 70 75 80	
	GTC ATC ATA GAG GAA GGG AAG TAC TCC CTG GTG ATG GAG TAC ATG GAG	288
	Val Ile Ile Glu Glu Gly Lys Tyr Ser Leu Val Met Glu Tyr Met Glu	
	85 90 95	
20	AAG GGC AAC CTG ATG CAC GTG CTG AAA GCC GAG ATG AGT ACT CCG CTT	336
	Lys Gly Asn Leu Met His Val Leu Lys Ala Glu Met Ser Thr Pro Leu	
	100 105 110	
	TCT GTA AAA GGA AGG ATA ATT TTG GAA ATC ATT GAA GGA ATG TGC TAC	384
	Ser Val Lys Gly Arg Ile Ile Leu Glu Ile Ile Glu Gly Met Cys Tyr	
25	115 120 125	
	TTA CAT GGA AAA GGC GTG ATA CAC AAG GAC CTG AAG CCT GAA AAT ATC	432
	Leu His Gly Lys Gly Val Ile His Lys Asp Leu Lys Pro Glu Asn Ile	
	130 135 140	
30	CTT GTT GAT AAT GAC TTC CAC ATT AAG ATC GCA GAC CTC GGC CTT GCC	480
	Leu Val Asp Asn Asp Phe His Ile Lys Ile Ala Asp Leu Gly Leu Ala	
	145 150 155 160	
	TCC TTT AAG ATG TGG AGC AAA CTG AAT AAT GAA GAG CAC AAT GAG CTG	528
	Ser Phe Lys Met Trp Ser Lys Leu Asn Asn Glu Glu His Asn Glu Leu	
	165 170 175	
35	AGG GAA GTG GAC GGC ACC GCT AAG AAG AAT GGC GGC ACC CTC TAC TAC	576
	Arg Glu Val Asp Gly Thr Ala Lys Lys Asn Gly Gly Thr Leu Tyr Tyr	
	180 185 190	
	ATG GCG CCC GAG CAC CTG AAT GAC GTC AAC GCA AAG CCC ACA GAG AAG	624
	Met Ala Pro Glu His Leu Asn Asp Val Asn Ala Lys Pro Thr Glu Lys	
40	195 200 205	
	TCC GAT GTG TAC AGC TTT GCT GTA GTA CTC TGG GCG ATA TTT GCA AAT	672
	Ser Asp Val Tyr Ser Phe Ala Val Val Leu Trp Ala Ile Phe Ala Asn	
	210 215 220	
	AAG GAG CCA TAT GAA AAT GCT ATC TGT GAG CAG CAG TTG ATA ATG TGC	720

	AAC AAT GGA TTA TAT AGC TCA CAT GGC TTT GGA ACA AGA CCA CTG GAT	1440
	Asn Asn Gly Leu Tyr Ser Ser His Gly Phe Gly Thr Arg Pro Leu Asp	
	465 470 475 480	
	CCA GGA ACA GCA GGT CCC AGA GTT TGG TAC AGG CCA ATT CCA AGT CAT	1488
5	Pro Gly Thr Ala Gly Pro Arg Val Trp Tyr Arg Pro Ile Pro Ser His	
	485 490 495	
	ATG CCT AGT CTG CAT AAT ATC CCA GTG CCT GAG ACC AAC TAT CTA GGA	1536
	Met Pro Ser Leu His Asn Ile Pro Val Pro Glu Thr Asn Tyr Leu Gly	
	500 505 510	
10	AAT ACA CCC ACC ATG CCA TTC AGC TCC TTG CCA CCA ACA GAT GAA TCT	1584
	Asn Thr Pro Thr Met Pro Phe Ser Ser Leu Pro Pro Thr Asp Glu Ser	
	515 520 525	
	ATA AAA TAT ACC ATA TAC AAT AGT ACT GGC ATT CAG ATT GGA GCC TAC	1632
	Ile Lys Tyr Thr Ile Tyr Asn Ser Thr Gly Ile Gln Ile Gly Ala Tyr	
15	530 535 540	
	AAT TAT ATG GAG ATT GGT GGG ACG AGT TCA TCA CTA CTA GAC AGC ACA	1680
	Asn Tyr Met Glu Ile Gly Gly Thr Ser Ser Ser Leu Leu Asp Ser Thr	
	545 550 555 560	
	AAT ACG AAC TTC AAA GAA GAG CCA GCT GCT AAG TAC CAA GCT ATC TTT	1728
20	Asn Thr Asn Phe Lys Glu Glu Pro Ala Ala Lys Tyr Gln Ala Ile Phe	
	565 570 575	
	GAT AAT ACC ACT AGT CTG ACG GAT AAA CAC CTG GAC CCA ATC AGG GAA	1776
	Asp Asn Thr Thr Ser Leu Thr Asp Lys His Leu Asp Pro Ile Arg Glu	
	580 585 590	
25	AAT CTG GGA AAG CAC TGG AAA AAC TGT GCC CGT AAA CTG GGC TTC ACA	1824
	Asn Leu Gly Lys His Trp Lys Asn Cys Ala Arg Lys Leu Gly Phe Thr	
	595 600 605	
	CAG TCT CAG ATT GAT GAA ATT GAC CAT GAC TAT GAG CGA GAT GGA CTG	1872
	Gln Ser Gln Ile Asp Glu Ile Asp His Asp Tyr Glu Arg Asp Gly Leu	
30	610 615 620	
	AAA GAA AAG GTT TAC CAG ATG CTC CAA AAG TGG GTG ATG AGG GAA GGC	1920
	Lys Glu Lys Val Tyr Gln Met Leu Gln Lys Trp Val Met Arg Glu Gly	
	625 630 635 640	
	ATA AAG GGA GCC ACG GTG GGG AAG CTG GCC CAG GCG CTC CAC CAG TGT	1968
35	Ile Lys Gly Ala Thr Val Gly Lys Leu Ala Gln Ala Leu His Gln Cys	
	645 650 655	
	TCC AGG ATC GAC CTT CTG AGC AGC TTG ATT TAC GTC AGC CAG AAC	2013
	Ser Arg Ile Asp Leu Leu Ser Ser Leu Ile Tyr Val Ser Gln Asn	
	660 665 670	
40	TAA	2016

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 671 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

5 Met Gln Pro Asp Met Ser Leu Asn Val Ile Lys Met Lys Ser Ser Asp
1 5 10 15
Phe Leu Glu Ser Ala Glu Leu Asp Ser Gly Gly Phe Gly Lys Val Ser
20 25 30
10 Leu Cys Phe His Arg Thr Gln Gly Leu Met Ile Met Lys Thr Val Tyr
35 40 45
Lys Gly Pro Asn Cys Ile Glu His Asn Glu Ala Leu Leu Glu Glu Ala
50 55 60
Lys Met Met Asn Arg Leu Arg His Ser Arg Val Val Lys Leu Leu Gly
65 70 75 80
15 Val Ile Ile Glu Glu Gly Lys Tyr Ser Leu Val Met Glu Tyr Met Glu
85 90 95
Lys Gly Asn Leu Met His Val Leu Lys Ala Glu Met Ser Thr Pro Leu
100 105 110
20 Ser Val Lys Gly Arg Ile Ile Leu Glu Ile Ile Glu Gly Met Cys Tyr
115 120 125
Leu His Gly Lys Gly Val Ile His Lys Asp Leu Lys Pro Glu Asn Ile
130 135 140
Leu Val Asp Asn Asp Phe His Ile Lys Ile Ala Asp Leu Gly Leu Ala
145 150 155 160
25 Ser Phe Lys Met Trp Ser Lys Leu Asn Asn Glu Glu His Asn Glu Leu
165 170 175
Arg Glu Val Asp Gly Thr Ala Lys Lys Asn Gly Gly Thr Leu Tyr Tyr
180 185 190
Met Ala Pro Glu His Leu Asn Asp Val Asn Ala Lys Pro Thr Glu Lys
30 195 200 205
Ser Asp Val Tyr Ser Phe Ala Val Val Leu Trp Ala Ile Phe Ala Asn
210 215 220
Lys Glu Pro Tyr Glu Asn Ala Ile Cys Glu Gln Gln Leu Ile Met Cys
225 230 235 240
35 Ile Lys Ser Gly Asn Arg Pro Asp Val Asp Asp Ile Thr Glu Tyr Cys
245 250 255
Pro Arg Glu Ile Ile Ser Leu Met Lys Leu Cys Trp Glu Ala Asn Pro
260 265 270
40 Glu Ala Arg Pro Thr Phe Pro Gly Ile Glu Glu Lys Phe Arg Pro Phe
275 280 285
Tyr Leu Ser Gln Leu Glu Glu Ser Val Glu Glu Asp Val Lys Ser Leu
290 295 300
Lys Lys Glu Tyr Ser Asn Glu Asn Ala Val Val Lys Arg Met Gln Ser
305 310 315 320

	Leu	Gln	Leu	Asp	Cys	Val	Ala	Val	Pro	Ser	Ser	Arg	Ser	Asn	Ser	Ala
					325					330				335		
	Thr	Glu	Gln	Pro	Gly	Ser	Leu	His	Ser	Ser	Gln	Gly	Leu	Gly	Met	Gly
				340					345					350		
5	Pro	Val	Glu	Glu	Ser	Trp	Phe	Ala	Pro	Ser	Leu	Glu	His	Pro	Gln	Glu
			355					360					365			
	Glu	Asn	Glu	Pro	Ser	Leu	Gln	Ser	Lys	Leu	Gln	Asp	Glu	Ala	Asn	Tyr
		370					375					380				
10	His	Leu	Tyr	Gly	Ser	Arg	Met	Asp	Arg	Gln	Thr	Lys	Gln	Gln	Pro	Arg
	385					390				395						400
	Gln	Asn	Val	Ala	Tyr	Asn	Arg	Glu	Glu	Glu	Arg	Arg	Arg	Arg	Val	Ser
				405						410				415		
	His	Asp	Pro	Phe	Ala	Gln	Gln	Arg	Pro	Tyr	Glu	Asn	Phe	Gln	Asn	Thr
			420						425					430		
15	Glu	Gly	Lys	Gly	Thr	Val	Tyr	Ser	Ser	Ala	Ala	Ser	His	Gly	Asn	Ala
			435					440					445			
	Val	His	Gln	Pro	Ser	Gly	Leu	Thr	Ser	Gln	Pro	Gln	Val	Leu	Tyr	Gln
		450					455					460				
20	Asn	Asn	Gly	Leu	Tyr	Ser	Ser	His	Gly	Phe	Gly	Thr	Arg	Pro	Leu	Asp
	465				470					475						480
	Pro	Gly	Thr	Ala	Gly	Pro	Arg	Val	Trp	Tyr	Arg	Pro	Ile	Pro	Ser	His
				485						490				495		
	Met	Pro	Ser	Leu	His	Asn	Ile	Pro	Val	Pro	Glu	Thr	Asn	Tyr	Leu	Gly
			500						505					510		
25	Asn	Thr	Pro	Thr	Met	Pro	Phe	Ser	Ser	Leu	Pro	Pro	Thr	Asp	Glu	Ser
		515					520						525			
	Ile	Lys	Tyr	Thr	Ile	Tyr	Asn	Ser	Thr	Gly	Ile	Gln	Ile	Gly	Ala	Tyr
		530				535						540				
30	Asn	Tyr	Met	Glu	Ile	Gly	Gly	Thr	Ser	Ser	Ser	Leu	Leu	Asp	Ser	Thr
	545				550					555						560
	Asn	Thr	Asn	Phe	Lys	Glu	Glu	Pro	Ala	Ala	Lys	Tyr	Gln	Ala	Ile	Phe
				565					570					575		
	Asp	Asn	Thr	Thr	Ser	Leu	Thr	Asp	Lys	His	Leu	Asp	Pro	Ile	Arg	Glu
			580					585						590		
35	Asn	Leu	Gly	Lys	His	Trp	Lys	Asn	Cys	Ala	Arg	Lys	Leu	Gly	Phe	Thr
		595					600						605			
	Gln	Ser	Gln	Ile	Asp	Glu	Ile	Asp	His	Asp	Tyr	Glu	Arg	Asp	Gly	Leu
		610					615					620				
40	Lys	Glu	Lys	Val	Tyr	Gln	Met	Leu	Gln	Lys	Trp	Val	Met	Arg	Glu	Gly
	625				630					635						640
	Ile	Lys	Gly	Ala	Thr	Val	Gly	Lys	Leu	Ala	Gln	Ala	Leu	His	Gln	Cys
				645					650					655		
	Ser	Arg	Ile	Asp	Leu	Leu	Ser	Ser	Leu	Ile	Tyr	Val	Ser	Gln	Asn	
			660						665					670		